

GenCore version 5.1.4\_p5\_4578  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: March 15, 2003, 15:07:49 ; Search time 74.0238 Seconds  
(without alignments)  
1537.035 Million cell updates/sec

Title: US-08-978-217-16

Perfect score: 1985  
Sequence: 1 MATCEISNVFSNFMNAYS.....YKFGKNSGCKEKEVEGSEN 371

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n model -DBV=ldp  
-Q/cgn2\_1/USFTO.spool/US08978217/runat.14032003.141838.13457/app.query.fasta\_1.1500  
-DB=Issued\_Patents\_NA -QFMT=IsaStep -SUFFIX=tni -MINMATCH=0.1 -LOOPECL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US08978217 @CNC 1.131 @runat.14032003.141838.13457 -NCPU=6 -ICPU=3  
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-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*  
1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCUTS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1712	86.2	1920	1	US-08-746-789A-1
2	586	29.5	5427	3	US-09-009-913-2
3	580	29.2	5510	3	US-09-009-913-3
4	580	29.2	5667	3	US-09-009-913-4
5	543	27.4	852	4	US-09-020-956-44
6	543	27.4	852	4	US-09-030-607-44
7	543	27.4	852	4	US-09-605-785-44
8	543	27.4	852	4	US-09-439-313-44
9	543	27.4	852	4	US-09-352-616A-44
10	543	27.4	852	4	US-09-232-149A-44
11	507	25.5	848	3	US-09-009-913-338
12	435.5	21.9	2280	3	US-09-009-913-8

13	435.5	21.9	2428	3	US-09-009-913-6	Sequence 6, Appl1
14	435.5	21.9	2498	3	US-09-009-913-10	Sequence 10, Appl1
15	238.5	12.0	2975	1	US-08-368-281-1	Sequence 1, Appl1
16	238.5	12.0	3240	1	US-08-368-281-3	Sequence 3, Appl1
17	234.5	11.8	1528	4	US-08-878-177-3	Sequence 3, Appl1
18	233.5	11.8	1905	4	US-09-055-113-2	Sequence 2, Appl1
19	225.5	11.4	1604	1	US-08-306-691B-43	Sequence 43, Appl1
20	225.5	11.4	1604	5	PCT-US93-06251-9	Sequence 9, Appl1
21	225	11.3	1447	4	US-08-878-177-1	Sequence 1, Appl1
22	225	11.3	2388	2	US-08-343-443B-3	Sequence 3, Appl1
23	220	11.1	2268	3	US-09-344-579-1	Sequence 1, Appl1
24	214	10.8	1752	4	US-09-360-779-1	Sequence 1, Appl1
25	214	10.8	1752	4	US-09-435-335-1	Sequence 1, Appl1
26	202.5	10.2	2266	2	US-09-213-767-1	Sequence 1, Appl1
27	180.5	9.1	2667	4	US-08-469-412A-1	Sequence 1, Appl1
28	180.5	9.1	2667	4	US-09-021-715-1	Sequence 1, Appl1
29	179	9.0	2410	2	US-08-780-835B-1	Sequence 1, Appl1
30	179	9.0	2410	4	US-09-303-268-1	Sequence 1, Appl1
31	179	9.0	2410	4	US-09-116-049-1	Sequence 1, Appl1
32	177	8.9	2064	3	US-08-875-944B-1	Sequence 1, Appl1
33	177	8.9	2064	4	US-09-116-049-3	Sequence 3, Appl1
34	145.5	7.3	1364	1	US-08-306-691B-50	Sequence 50, Appl1
35	145.5	7.3	1364	5	PCT-US93-06251-65	Sequence 65, Appl1
36	125	6.3	2544	2	US-08-469-412A-6	Sequence 6, Appl1
37	125	6.3	2544	4	US-09-021-715-6	Sequence 6, Appl1
38	104	5.2	2344	3	US-08-893-852A-2	Sequence 2, Appl1
39	100	5.0	3783	4	US-08-506-296B-20	Sequence 20, Appl1
40	99.5	5.0	3848	2	US-08-808-931-14	Sequence 14, Appl1
41	99.5	5.0	3848	3	US-08-808-323-14	Sequence 14, Appl1
42	99.5	5.0	3848	3	US-09-050-603A-14	Sequence 14, Appl1
43	99.5	5.0	3848	4	US-09-102-420B-14	Sequence 14, Appl1
44	99.5	5.0	3848	3	US-09-497-698-14	Sequence 14, Appl1
45	98	4.9	1476	4	US-09-434-288-12	Sequence 12, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-746-789A-1  
; Sequence 1, Application US/08746789A  
; Patent No. 5789200  
; GENERAL INFORMATION:  
; APPLICANT: Ismail Kola, Martin J. Tymins, Christine DeBouck  
; TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELP3  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM 486  
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
; SOFTWARE: MICROSOFT WORD  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/746,789A  
; FILING DATE: No. 5789200el 15, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATG 50024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270 5219  
; TELEFAX: 610 270 4026  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 1920
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-08-746-789A-1

Alignment Scores:
Score: 1.3e-173 Length: 1920
Percent Similarity: 92.74% Matches: 323
Best Local Similarity: 86.83% Conservative: 22
Query Match: 86.25% Indels: 25
Gaps: 2

US-08-978-217-16 (1-371) x US-08-746-789A-1 (1-1920)

Qy 1 MetAlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMetTyrSer 20
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Qy 21 SerGluAProThrLeuAlaProAlaProPro---ThrThrPheGlyThrGluAspLeu 39
Db 175 TCGGAGGACTCCACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 234

Qy 40 ValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGlyProGluIleAlaSerTyrThr 59
Db 235 GTACTGACCTGAGCAACCCCGAGATGATGAGAGGAGACAGAAAGGCTGAGCTTG 294

Qy 60 SerGluAProGlnPheTyrSerTyrThrGlnValLeuGluTyrIleSerTyrGlnVal 79
Db 295 GGGGAACAGCCCACTGCTGCTGCAAGAGCAGGTTTGTGATGATGATGATGATGATGATG 354

Qy 80 GluIleAsnIleTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspIleAla 99
Db 355 GAGAGAAACAAGTACGACGCAAGCCGCACTGCTTCAAGATGACATGATGATGATGATG 414

Qy 100 ThrLeuCysSerCysAlaLeuGluIleLeuArgLeuValPheGlyProLeuGlyAspGln 119
Db 415 ACCCTCTGCAATTTGCTTGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 474

Qy 120 LeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTyrIleIle 139
Db 475 CTCCATGCCAGCTCGAGACTCCTCACTTCCAGCTTGTGATGATGATGATGATGATGAT 534

Qy 140 GluLeuLeuGluIleAspGlyMetSerPheGlnGlnIleGlnIleGlnIleGlnIle 159
Db 535 GAGCTGCTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 591

Qy 160 AspGlnGlySerProPheAlaGlnGlnIleLeuAspAspGlyArgGlnAlaSerProTyr 179
Db 592 GACCAAGGCAAGCCCTTGTGAGAGCTGCTGAGAGAGCTGACAGAGCCAGCCCTTAC 651

Qy 180 TyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSerThrAla 199
Db 652 CACCCGCGAGCTGAGCGCAGAGAGCCCTTCCCTGAGAGCTTGAAGCTTCCACCGCA 711

Qy 200 ArgThrAlaThrProGlnSerSerThrAlaSerAspSerGlyIleSerAspValAspLeu 219
Db 712 GGGACTGTGCTTCTCGGAGCTCCCACTCTCACTCGAGCTCGAGTGAAGTGAAGTGAAG 771

Qy 220 AspLeuThrGluSerIleValPheProArgAspAspPheThrAspTyrIleValGlySer 239
Db 772 GATCCCACTGATGCGCAAGCTTCTCCCGCAGATGCTTTTCGATGATGATGATGATGAT 831

Qy 240 ProIleHisGlyIleValArgIleArgIleArgProArgIleValSerIleValIleTyrPhe 259
Db 832 CCGAAGCAACGGGAAGCGGAAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 891

Qy 260 CysLeuGluGlyIleValIleSerIleHisAlaProArgGlyThrHisLeuTyrGluPheIle 279
Db 892 TGTCTCGAGGCGCAAGAGCAAGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 951
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Qy 280 ArgAspIleLeuIleHisProGluLeuAsnGluIleLeuMetIleTyrPheGluAsnArgHis 299
Db 952 CGGAGCATCTTCATCCACCGGAGCTCAACGAGGCGCTCATGAGTGGAGAAATCGGCAT 1011

Qy 300 GluGlyValPheIleValPheLeuArgSerGluAlaValAlaGlnLeuTyrPheGlnIleVal 319
Db 1012 GAAGCGCTTCAAGTTCCTGCGCTCCGAGGCTGTGCGCCCAACTATAGGGGCAAAAGAA 1071

Qy 320 LysAsnSerAsnMetTyrTyrGluIleLeuSerArgAlaMetArgTyrTyrTyrIleValArg 339
Db 1072 AAGAAGCAACATGACTTACGAGAGCTGAGAGCCGCGCGCATGAGTACTTACAAACG 1131

Qy 340 GluIleLeuGluArgValAlaAspGlyArgArgIleValTyrIleValIleValIleVal 359
Db 1132 GAGATCTCGAAGCGGTGAGTGGCGCGGAGCTCGTCTACAAAGTTTGGCAAAACTCAAGC 1191

Qy 360 GlyTyrPheGluGluGluValAlaGlyIleSerArgAsn 371
Db 1192 GCGTGAAGAGGAAAGAGTTCCTCAGATGCGAAGC 1227

RESULT 2
US-09-009-913-2
; Sequence 2, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axy's Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009, 913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5427 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-009-913-2

Alignment Scores:
Pred. No.: 2.58e-52 Length: 5427
Score: 586.00 Matches: 51
Percent Similarity: 50.26% Conservative: 141
Best Local Similarity: 36.91% Mismatches: 86
Query Match: 29.52% Indels: 104
Gaps: 11

US-08-978-217-16 (1-371) x US-09-009-913-2 (1-5427)
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Db 536 CAGCTCCTCTACAGCACTGTGAGCATCTGAGGTGAAGCGGACAGTGCATGAC--- 592
Qy 135 LeuSerTrpIleIleGlnLeuLeuGlnLysAspGlyMetSerPheGlnGluSerLeuGly 154
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 593 -----CTGTTCACAGCCACACACAAAT 613
Qy 155 AspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuAspAspGlyArg 174
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 614 GTCATTGTCAAGACTGAAACAACTGAGCT-----TCCATCATGAACACCTGGAAA 664
Qy 175 GlnAlaSerProTyrTyrCysSerThrTyrGlyArgProGlyAlaProSerProGlySerSer 194
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Db 665 GACGAGAACTATTATTATGACCAACTATGTT----- 697
Qy 195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGly 214
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Db 698 -----AGCACA----- 703
Qy 215 SerAspValAspLeuAspLeuThrGlnSerLysValPheProArgAspAspPhe----- 232
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Db 704 -----GTAGATTGTGGACAGCAAACTTCTGCGGAGCTTCAGATCTCCATG 751
Qy 233 -----ThrAspTyrLysLysGlyGluProLysHisGlyLysAspGlyAspGlyArg 249
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Db 752 ACAACACACAGTACCTTCTGTCAGAGTCACTGATGATGAAAGAGACAGACCC 811
Qy 250 ProArgLysLeuSerLysGlyTyrTrpAspCysLeuGlnGlyLysLysSerLysHisAla 269
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 812 CCGCCCAAGTGCACACCA-----AAGCACAAC 841
Qy 270 ProArgGlyThrHisLeuTrpGlnPheIleArgAspIleLeuHisAspProGluLeuAsn 289
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Db 842 CCGAAGAGGAGTCACTTATGGAATTCATCCGCGACATCTCTTGAACCCAGACAAAC 901
Qy 290 GlnGlyLeuMetLysTrpGlnLysAsnArgHisGlnGlyValPheLysPheLeuArgSerGlu 309
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 902 CCAGATTTAATAAATGGAGAACCGATGAGGGCTTTCAGGCTTTGAAATCAGAG 961
Qy 310 AlaValAlaGlnLeuTrpGlnLysLysLysAsnSerAspMetThrTyrGlnLysLeu 329
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Db 962 CGAGTGGCTCACCTATGGGGTAAAAAGAACACACAGCATGACCTATGAAAAAGCTC 1021
Qy 330 SerArgAlaMetArgTyrTyrTyrLysArgGlnIleLeuGlnArgValAspGlyArgArg 349
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Db 1022 AGCCGAGCTATGATATTACTTACAAAGAGAAATATCTGAGCGTGTGGATGACGAA 1081
Qy 350 LeuValTyrLysPheGlyLysAsnSerSerGlyTyrLysGlnGlnGlu 365
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Db 1082 CTGCTATTATTAATTTGGAGAAATGCCCGAGGATGAGAGAAATGAA 1129

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5667 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-009-913-4

Alignment Scores:
Pred. No.: 1,21e-51 Length: 5667
Score: 580.00 Matches: 129
Percent Similarity: 54.43% Conservative: 43
Best Local Similarity: 40.82% Mismatches: 78
Query Match: 29.22% Indels: 66
DB: 3 Gaps: 7

US-08-978-217-16 (1-371) x US-09-009-913-4 (1-5667)
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Db 513 TGGCATGAATATTCCTTCAGTACTGACCAAGTACAGGAGTGGAGTGCCTCCAGCAC 572
Qy 78 GlnValGlnLysAsnLysTyrAspAlaSerSerLysAspPheSerArgCysAsnMetAsp 97
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 573 CTCCTGACACCAACACAGCTGATGCCAATTGTATCCTTTCCAAGATTGACATCAAC 632
Qy 98 GlyAlaThrLeuCysSerCysAlaLeuGlnLeuArgLeuValPheGlyProLeuGly 117
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 633 GCGGAGCACCTCTGACGATGAGTTGACGAGATTCAACCCGCGCGACGCGCGGG 692
Qy 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsn-----SerSerAspGlu 134
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 693 CAGCTCCTCTACAGCACTTGCAGCATCTGAAGTGAACGGCCAGTGCAGTAGTAC-- 749
Qy 135 LeuSerTrpIleIleGlnLeuLeuGlnLysAspGlyMetSerPheGlnGluSerLeuGly 154
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 750 -----CTGTTCACAGTCCACACAAAT 770
Qy 155 AspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLeuAspAspGlyArg 174
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 771 GTCATTGTCAAGACTGAAACAACTGAGCT-----TCCATCATGAACACCTGGAAA 821
Qy 175 GlnAlaSerProTyrTyrCysSerThrTyrGlyArgProGlyAlaProSerProGlySerSer 194
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 822 GACGAGAACTATTATTATGACCAACTATGTT----- 854
Qy 195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlyGly 214
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 855 -----AGCACA----- 860
Qy 215 SerAspValAspLeuAspLeuThrGlnSerLysValPheProArgAspAspPhe----- 232
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 861 -----GTAGATTGTGGAGACAGCAAACTTCTGCGGAGCTCAGATCTCCATG 908
Qy 233 -----ThrAspTyrLysLysGlyGluProLysHisGlyLysLysArgGlyArgGly 249
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 909 ACAACACACAGTACCTTCTGTTGACAGATCACTGATATGAAAGAGACAGAACCC 968

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QY 250 ProArgIysLeuSerIysGluTyrTrpAspCysLeuGluGlyIysIysSerIysHisAla 269  
 DB CCGCCAAAGTGCCACACCAAA-----AACCAACAAC 998  
 QY 270 ProArgIysThrHisLeuTrpGlnPheIleArgAspIleLeuIleHisProGluLeuAsn 289  
 DB 999 CCGAGAGGAGCTACCTATGGAATTCATCCGACATCCCTTGAACCCAGACAAAGAAC 1058  
 QY 290 GlnGlyLeuMetCysTrpGluAsnArgHisGluGlyValPheIysPheLeuArgSerGlu 309  
 DB 1059 CCGAGATTATATAAATGGAGAGACCATCTGAGGCGCTCTTCAAGTCTTGAATCAAG 1118  
 QY 310 AlaValAlaGlnLeuTrpGlyGlnIysIysIysAsnSerAsnMetThrTyrGlyIysLeu 329  
 DB 1119 GCAGTGCTCAGCATGCGGGTAAAGAAAGAACACAGCAGCATGACCTATGAAAGCTC 1178  
 QY 330 SerArgAlaMetArgIysTyrTyrIysArgGlnIleLeuGluValAspGlyArg 349  
 DB 1179 AGCGAGCTTATGAGATTTACTACAAAGAAATCTGGAGCTGTGATGAGCAAGA 1238  
 QY 350 LeuValTyrIysPheGlyIysAsnSerSerGlyTyrIysGluGluGlu 365  
 DB 1239 CTGGTATATATAATTGGGAAGAAATGCCGAGATGAGAGAAATGAA 1286  
 RESULT 5  
 US-09-020-956-44/c  
 ; Sequence 44, Application US/09020956  
 ; Patent No. 6261562  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Jiangchun  
 ; APPLICANT: Dillin, Davin C.  
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO  
 ; NUMBER OF SEQUENCES: 178  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED and BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/020,956  
 ; FILING DATE: 09-FEB-1998  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Maki, David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 210121.42762  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 852 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; US-09-020-956-44  
 Alignment Scores:  
 Pred. No.: 5.98e-49 Length: 852  
 Score: 543.00 Matches: 124  
 Percent Similarity: 54.28% Conservative: 41  
 Best Local Similarity: 40.79% Mismatches: 73

Query Match: 27.36% Indels: 66  
 DB: 4 Gaps: 7  
 US-08-978-217-16 (1-371) x US-09-020-956-44 (1-852)  
 QY 70 GlnValLeuGluTrpIleSerTyrGlnValGlnIlyAsnIysTyrAspAlaSerIle 89  
 DB 850 CAGGTGTGGAGAGGCTCCACATCTCCCTGGACCAACCAAGTGGATGGCAATTGATC 791  
 QY 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluLeu 109  
 DB 790 CTTTCCANAGTTCCACATCAACGGCGAGACACTTTGGCAGCATGACTTTGGAGACTC 731  
 QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuIleHisAlaGlnLeuArgAspLeuThrSer 129  
 DB 730 ACCCGGGCGGACAGGAGCGGGGCAANNCTCCTCAACGAACTTGGAGCATCTGAAGTGG 671  
 QY 130 Asn-----SerSerArgGluLeuSerTrpIleIleGluLeuGluIlyAspGly 146  
 DB 670 AACGGCCAGTCAGTGTGAC----- 650  
 QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166  
 DB 649 ---CTGTTCCAGTCCACACCAATGTCATTGTCAAGACTGAACAACTGAGCT- 599  
 QY 167 GlnGluLeuLeuAspArgIysArgAlaIleSerProTyrTyrCysSerThrTyrGlyPro 186  
 DB 598 ---TCCATCATGAACACCTGGAAAGACNAGACTATTATATGACCACTATGCT- 545  
 QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206  
 DB 544 -----AGCACA----- 539  
 QY 207 SerHisAlaSerAspSerGlyIysSerAspValAspLeuAspLeuThrGluSerIysVal 226  
 DB 538 -----GTACATTTGTTGGACAGCAAACT 515  
 QY 227 PheProArgAspAspPhe-----ThrAspTyrIysIysGlyProIys 241  
 DB 514 TTCGCCGGGCTCAGATCTCCATGACCAACACCAAGTCACTTCTGTGAGAGTCACT 455  
 QY 242 HisGlyIysArgIysArgIysArgProArgIysLeuSerIysGluTyrTrpAspCysLeu 261  
 DB 454 GATATGAAAAAGAGACAGACCCCTCCCAAGTGCACACCAAA----- 410  
 QY 262 GlnGlyIysIysSerIysHisAlaProArgGlyThrHisLeuTrpGlnPheIleArgAsp 281  
 DB 409 -----AAGCACAACCCGAGAGGACTCTATTATGGGAATTCATCCGAC 365  
 QY 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetCysTrpGluAsnArgHisGluGly 301  
 DB 364 ATCTCTTGAACCCAGACCAAGAACCCAGATTAATAAATGGGAAGCCGATCTGAGGCG 305  
 QY 302 ValPheIysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnIysIysAsn 321  
 DB 304 GTCTTCAGTTCTTGAATATCAGAGGAGTGTGCTCAGCTATGGGTTAAAGAAACAAC 245  
 QY 322 SerAsnMetThrTyrGlyIysLeuSerArgAlaMetArgIysTyrTyrIysAspGluIle 341  
 DB 244 AGCAGCATGACCTATGAAAGCTCAGCGGCTATGAGATTAATTAACAAAGAAATTT 185  
 QY 342 LeuGluArgValAspGlyArgLeuValTyrIysPheGlyIysAsnSerSerGlyTyr 361  
 DB 184 CTGGAGCGTGTGATGACCAAGACTGTATATAATTGGGAAGAAATGCCAGAGATGG 125  
 QY 362 LysGluGluGlu 365  
 DB 124 AGAGAAATGAA 113  
 RESULT 6  
 US-09-030-607-44/c  
 ; Sequence 44, Application US/09030607  
 ; Patent No. 6262245

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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030.607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 852 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-030-607-44

Alignment Scores:
Pred. No.: 5,98e-49 Length: 852
Score: 543.00 Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73
Query Match: 27.36% Indels: 66
DB: 4 Gaps: 7

US-08-978-217-16 (1-371) x US-09-030-607-44 (1-852)
Qy 70 GlnValLeuGluTrpIleSerTyrglnValAlaGluLysAsnLysTyAspAlaSerSerIle 89
Db ||||| ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 850 CAGGTGTGGAGATGGCTCATCATCACTCCGACACCAACCACTGATGTCGAATTGTATC 791
Qy 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCySerCysAlaLeuGluGluLeu 109
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 790 CCTTCCAGAGTTCGATCATCAACGCGGACGACCTTTCGAGCATGATTTGACGAGATTTC 731
Qy 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 730 ACCCGGCGCGGACGAGCGGCGGACCTCTCTACAGCACTTGACGATGCAAGTGG 671
Qy 130 Aen-----SerSerAspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGly 146
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 670 AACGGCCAGTGCATGATGAC----- 650
Qy 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 649 ---CTGTTCAGTCCACACACATGTCATTTGCAAGACTGACCAAACTGAGCCT----- 599
Qy 167 GlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyTrpCySerThrTyArgIlePro 186
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 598 ---TCCATCATGACACCTGGAAGACNAGAACTATTATATGACCAACCAATATGTT--- 545

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Qy 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 544 -----AGCACA----- 539
Qy 207 SerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSerLysVal 226
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 538 -----GTAGATTGTGGACAGCAAACT 515
Qy 227 PheProArgAspAspPhe-----ThrAspTyTrpLysGlyGluProLys 241
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 514 TTCTGCGCGGCTCAGATCTCCATGACCAACCAACGATCCTCTGTTGACGATGACCT 455
Qy 242 HisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyTrpAspCysLeu 261
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 454 GATATGAAAAAGAGCAAGACCCCTCCCAAGTGCACACCAAA----- 410
Qy 262 GluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAsp 281
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 409 -----AGCACACCCGAGAGGAGCTCATATGGGAATTCATCCGCGAC 365
Qy 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGly 301
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 364 ATCCTTTCGAACCCAGACACCAACCAACGATTAATAATGGAAAGACCATCTGAGGGC 305
Qy 302 ValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsn 321
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 304 GTCTTCAGGTTCTTGAATTCAGAGGCAAGTGGCTCAGCTATGGGTAAAGAAAGAACAC 245
Qy 322 SerAsnMetThrTyrglnLysLeuSerArgHisMetArgTyTrpTyTrpLysArgGluIle 341
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 244 AGCAGCATGACCTATGAAAGACCTCAGCGAGCTATGAGATTAATCTACAAAGAGAAATT 185
Qy 342 LeuGluArgValAspGlyArgArgLeuValTyTrpLysPheGlyLysAsnSerSerGlyTrp 361
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 184 CTGAGAGCTGTGATGACGAGAGACTGATATATAATTGGGAAGAAATGCCCGAGATGG 125
Qy 362 LysGluGluGlu 365
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db 124 AGAGAAATGAA 113

RESULT 7
US-09-605-785-44/C
Sequence 44, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605.785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 44
LENGTH: 852
TYPE: DNA
ORGANISM: Homo sapien

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FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(852)
; OTHER INFORMATION: n = A,T,C or G
US-09-605-785-44

Alignment Scores:
Pred. No.: 5,98e-49 Length: 852
Score: 543.00 Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73
Query Match: 27.36% Indels: 66
DB: Gaps: 7

US-08-978-217-16 (1-371) x US-09-605-785-44 (1-852)
QY 70 GlnValLeuGluTrpLieserTyrgInValGluLeuAsnTyrrAspAlaSerSerIle 89
DB 850 CAGGTGTGGAGTGGCTCCATCCTCTGACACCAACGCTGATGCAATTGTATC 791
QY 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluLeu 109
DB 790 CTTTCCANAGTTCCACATCAACGCGAGACCTTTGCACATGAGTTGCGAGATTC 731
QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129
DB 730 ACCCGGCGGAGGAGCGCGGCGCANCCTCTACAGCAACTTGACAGCATCTGAATGG 671
QY 130 Asn-----SerSerAspGluLeuSerTrpIleIleGluLeuGluValAspGly 146
DB 670 AACGGCCAGTGCAGTACTGAC----- 650
QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
DB 649 ---CTGTTCCAGTCCACACACATGTCATGTCACAGCTGAACAACTGAGCT- 599
QY 167 GlnGluLeuLeuAspAspArgGlyArgGlnAlaSerProTyrrCysSerThrTyrrGlyPro 186
DB 598 ---TCCATCATGAACACCTCGAAGACNAGAACTATTATATGACACCACTATGCT- 545
QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206
DB 544 -----AGCACA----- 539
QY 207 SerHisAlaSerAspSerArgGlySerAspValAspLeuAspLeuThrGlnSerIleVal 226
DB 538 -----GTAGATTGTTGGACAGCAAACT 515
QY 227 PheProArgAspAspPhe-----ThrAspTyrrLysLysGlyGluProLys 241
DB 514 TTCTGCCGGGCTCGATCTCCATGACAAACCACTGACCTTCTGTTGCAGACTCACT 455
QY 242 HisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyrrPASPcysLeu 261
DB 454 GATATGAAAAAGGAGCAAGCCCTCGCCCAAGTGCACACCAAA----- 410
QY 262 GlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAsp 281
DB 409 -----AAGCAACAACCCGAGAGGACTCACTTATGGAATTATATCCGGGAC 365
QY 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGly 301
DB 364 ATCTCTTGAACCCAGACAGAACCCAGATTAATAATGGAAAGCCATCTGAGGGC 305
QY 302 ValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysAsn 321
DB 304 GTCTTCAGTTCCTTGAATCATGAGGAGTGGCTCAGCTATGGGGTAAAGAAACAAC 245
QY 322 SerAsnMetThrTyrrGluLysLeuSerArgAlaMetArgTyrrTyrrLysArgGluIle 341
DB 244 AGCAGCATGACCTTATGAAAAAGCTAGCCGAGCTATGAGATTTACTCAAAAGGAATT 185
QY 342 LeuGluLysValAspGlyArgArgLeuValTyrrLysPheGlyLysAsnSerSerGlyTrp 361

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DB 184 CTGAGCGTGTGATGAGACGAAAGCTGTATATTAATTGGGAAGATGCCGAGAGTGG 125
QY 362 LysGluGluGlu 365
DB 124 AGAGAAATGAA 113

RESULT 8
US-09-439-313-44/C
; Sequence 44, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kaloos, Gary
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(852)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-44

Alignment Scores:
Pred. No.: 5,98e-49 Length: 852
Score: 543.00 Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73
Query Match: 27.36% Indels: 66
DB: Gaps: 7

US-08-978-217-16 (1-371) x US-09-439-313-44 (1-852)
QY 70 GlnValLeuGluTrpLieserTyrgInValGluLeuAsnTyrrAspAlaSerSerIle 89
DB 850 CAGGTGTGGAGTGGCTCCATCCTCTGACACCAACGCTGATGCAATTGTATC 791
QY 90 AspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGluLeu 109
DB 790 CTTTCCANAGTTCCACATCAACGCGAGACCTTTGCACATGAGTTGCGAGATTC 731
QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129
DB 730 ACCCGGCGGAGGAGCGCGGCGCANCCTCTACAGCAACTTGACAGCATCTGAATGG 671
QY 130 Asn-----SerSerAspGluLeuSerTrpIleIleGluLeuGluValAspGly 146
DB 670 AACGGCCAGTGCAGTACTGAC----- 650
QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
DB 649 ---CTGTTCCAGTCCACACACATGTCATGTCACAGCTGAACAACTGAGCT- 599
QY 167 GlnGluLeuLeuAspAspArgGlyArgGlnAlaSerProTyrrCysSerThrTyrrGlyPro 186
DB 598 ---TCCATCATGAACACCTCGAAGACNAGAACTATTATATGACACCACTATGCT- 545

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Qy 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206
Db 544 -----AGCACA----- 539
Qy 207 SerHisAlaSerAspSerGlySerAspValAspLeuAspLeuThrGlnSerIleVal 226
Db 538 -----GTGATTTTGTGGACGCAAAACT 515
Qy 227 PheProArgAspAspPhe-----ThrAspTyrIleValGlyLupProlys 241
Db 514 TTCTGCGGGGCTCAGATCTCCATGACACCACGACCTTCTGTTGACAGATCAGCT 455
Qy 242 HisGlyLysArgLysArgGlyLysArgProArgLysLeuSerLysGlnTyrTrpAspCysLeu 261
Db 454 GATATGAAAAAGAGACAAAGACCCCTGCCAAGTGCACACAAA----- 410
Qy 262 GlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGlnPheIleArgAsp 281
Db 409 -----AAGCACAACCCGAGAGGAGACTCTTATGGAAATTCATCCGCGAC 365
Qy 282 IleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTrpGlnAsnArgHisGlnGly 301
Db 364 ATCTCTTGAACCCGACAGAAACCAGATTTAATAATGGAAAGACCGATCTGAGGCG 305
Qy 302 ValPheLysPheLeuArgSerGlnAlaValAlaGlnLeuTrpGlnLysLysIleAsn 321
Db 304 GTCTTCAGGTTCTTGAAATCAGAGGAGCTGCTCAGCTATGGGGTAAAAAGAAACAAAC 245
Qy 322 SerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlnIle 341
Db 244 AGCACAATGACCTATGAAAAAGCTCAGCCGATATGAGATATTAACAAAAAGAGAAATTT 185
Qy 342 LeuGlnArgValAspGlyLysArgLeuValTyrLysPheGlnLysAsnSerSerGlyTyr 361
Db 184 CTGGAGCGTGTGGATGAGCAAGAGACTGTATATTAATTTGGAAAGATCCCGAGAGATGG 125
Qy 362 LysGlnGlnGln 365
Db 124 AGAGAAATGAA 113

RESULT 9
US-09-352-616A-44/C
; Sequence 44, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352.616A
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(852)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-44

Alignment Scores:
Pred. No.: 5 98e-49 Length: 852
Score: 543.00 Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73

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Query Match: 27.36% Indels: 66
DB: 4 Gaps: 7
US-08-978-217-16 (1-371) x US-09-352-616A-44 (1-852)

Qy 70 GlnValLeuGlnTyrPheIleSerTyrGlnValGlnLysAsnLysTyrAspAlaSerSerIle 89
Db 850 CAGGTGTGGAGTGTGCTCATCTCCTCCTGAGACCAACCGCTGAGATGATTTATTC 791
Qy 90 AspPheSerArgCysAsnMetAspGlyValaThrLeuCysSerCysAlaLeuGlnGlnLeu 109
Db 790 CCTTTCANAGAGTTGACATACACGCGAGACCTTTGACACATGAGTTTCAGAGATTC 731
Qy 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSer 129
Db 720 ACCCGGCGGAGGAGCGCGGGCGANCTCCTTAACAGCACTTGACAGCATCTGAAGTGG 671
Qy 130 Asn-----SerSerAspGlnLeuSerTrpIleIleGlnLeuGlnLysAspGly 146
Db 670 AACGGCAGTCAGTATGAGC----- 650
Qy 147 MetSerPheGlnGlnLysSerLeuGlyAspLeuGlyProPheAspGlnLysProPheAla 166
Db 649 ---CTGTTCCAGTCCACACACAAATGCTATTGTCAAGACTGAACAAACTGAGCCT----- 599
Qy 167 GlnGlnLeuLeuAspAspGlyLysArgGlnAlaSerProTyrTyrCysSerThrTyrGlyPro 186
Db 598 ---TCCATCATGACACACCTGGAAAGACNAGAACTATTATATGACACCAACTATGGT--- 545
Qy 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206
Db 544 -----AGCACA----- 539
Qy 207 SerHisAlaSerAspSerGlyLysSerAspValAspLeuAspLeuThrGlnSerIleVal 226
Db 538 -----GTAGATTTGTTGGACAGCAAAACT 515
Qy 227 PheProArgAspAspPhe-----ThrAspTyrLysLysGlnLupProlys 241
Db 514 TTCTGCGGGGCTCAGATCTCCATGACAAACACAGTCACTTCTGTTGACAGATCAGCT 455
Qy 242 HisGlyLysArgLysArgGlyLysArgProArgLysLeuSerLysGlnTyrTrpAspCysLeu 261
Db 454 GATATGAAAAAGAGACAAAGACCCCTGCCAAGTGCACACAAA----- 410
Qy 262 GlnGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGlnPheIleArgAsp 281
Db 409 -----AAGCACAACCCGAGAGGAGACTCTTATGGAAATTCATCCGCGAC 365
Qy 282 IleLeuIleHisProGlnLeuAsnGlnGlyLeuMetLysTrpGlnAsnArgHisGlnGly 301
Db 364 ATCTCTTGAACCCGACAGAAACCAGATTTAATAATGGAAAGACCGATCTGAGGCG 305
Qy 302 ValPheLysPheLeuArgSerGlnAlaValAlaGlnLeuTrpGlnLysLysIleAsn 321
Db 304 GTCTTCAGGTTCTTGAAATCAGAGGAGCTGCTCAGCTATGGGGTAAAAAGAAACAAAC 245
Qy 322 SerAsnMetThrTyrGlnLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGlnIle 341
Db 244 AGCACAATGACCTATGAAAAAGCTCAGCCGAGCTATGAGATTTACTACAAAGAAATTT 185
Qy 342 LeuGlnArgValAspGlyLysArgLeuValTyrLysPheGlnLysAsnSerSerGlyTyr 361
Db 184 CTGGAGCGTGTGGATGAGCAAGAGACTGTATATTAATTTGGAAAGATGCCCGAGAGATGG 125
Qy 362 LysGlnGlnGln 365
Db 124 AGAGAAATGAA 113

RESULT 10
US-09-232-149A-44/C
; Sequence 44, Application US/09232149A
; Patent No. 6465611

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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232.149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(852)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-44

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Alignment Scores:
Pred. No.: 5.98e-49      Length: 852
Score: 543.00           Matches: 124
Percent Similarity: 54.28% Conservative: 41
Best Local Similarity: 40.79% Mismatches: 73
Query Match: 27.36%      Indels: 66
DB: 4                    Gaps: 7
US-08-978-217-16 (1-371) x US-09-232-149A-44 (1-852)

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QY 70 GlnValLeuGluTyrPilesSerTyrGlnValGluYsaNlySTYrAspAlaSerSerIle 89
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DB 850 CAGGTGTGGAGTGTGCTCCATCACCCTCTGTGACACCAACGCGATGCCAATTGATC 791
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 90 AspPheSerArgCySaamMetAspGlyAlaThrLeuCySerCySaAlaLeuGluGluLeu 109
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 790 CCTTCCAGATGTCGATCATCAACGCGAGCACTTGTGACAGATGATTTGACAGAGTTC 731
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 110 ArgLeuValPheGlyProLeuGlyAspGlnLeuHisAlaGlnLeuAspLeuThrSer 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 730 ACCCGGCGGCGGAGCGCGCGGCANCTCTCTACAGCAACTTGACAGCATTTAAAGTGG 671
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 130 Asn-----SerSerAspGluLeuSerTrpIleIleGluLeuGluYsaSpGly 146
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 670 AACGGCCAGTCAGTATGATGAC----- 650
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 147 MetSerPheGlnGluSerLeuGlyAspLeuGlyProPheAspGlnGlySerProPheAla 166
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 649 ---CTGTTCCAGTCCACACACAAATGTTGTCAAGACTGAACAACTGAGCCT----- 599
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 167 GlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyrTyrCySerThrTyrGlyPro 186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 598 ---TCCATCATGAACACTGTGAAGACNAGAACTATTATATGACCAACTATGCT--- 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 187 GlyAlaProSerProGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSer 206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 544 -----AGCACA----- 539
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 207 SerHisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSerIlyVal 226
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 538 -----GTAGATTGTTGGACAGCAAAACT 515
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 227 PheProArgAspAspPhe-----ThrAspTyrIlySlySlyGlyGluProlys 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 514 TTTCGCGCGGTCCAGATCTCCATGACCAACCACTCTCTCTGTGACAGATCAGCT 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 242 HisGlyIlySArgIlySArgGlyArgProArgIlySLeuSerIlyGluTyrTrpAspCysIeu 261
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 454 GATATGAAAAAGGACCAAGACCCCTCCCAAGTCCACACCAAA----- 410
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 262 GluGlyIlySlySerIlyHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAsp 281
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 409 -----AAGCAAAACCCGAGAGGAGCTTATTAGGAATTCATCCGGAC 365
QY 282 IleLeuIleHisProGluLeuAsnGluGlyLeuMetIlySTrpgIubAsnArgHisGluGly 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 364 ATCTCTTGAACCCAGACAGAACCCAGATTAATAAATGGGAAGCCATCTGAGGCG 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 302 ValPheIlySPhelLeuArgSerGlyAlaValAlaGlnLeuTrpGlyGlnIlySlySlyAsn 321
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 304 GTCTTCAGGTTCTTGAATCAGAGGAGCTGCTCAGCTATGGGGTAAAAAGAAACACAC 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 322 SerAspMetThrTyrGlyIlySLeuSerArgAlaMetArgTyrTyrTyrIlySArgGluIle 341
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 244 AGCAGCATGACCTATGAAAGCTCAGCCGAGCTATGATATTAATAAAGAAATTT 185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 342 LeuGluArgValAspGlyArgArgLeuValTyrIlySPhelIlySAsnSerSerGlyTyr 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 184 CTGAGCGCTGTGATGAGACCAAGACTGTATATAATTGGGAAGAAATGCCCGAGATGG 125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 362 IlySgluGluGlu 365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 124 AGAGAAATGAA 113
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 11
US-09-009-913-338
; Sequence 338, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axyx Pharmaceuticals, Inc.
; TITLE OF INVENTION: Asthma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 338:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...848
; OTHER INFORMATION:
US-09-009-913-338

Alignment Scores:
Pred. No.: 4.26e-45      Length: 848
Score: 507.00           Matches: 117

```

Percent Similarity: 52.70% Conservative: 39  
 Best Local Similarity: 39.53% Mismatches: 84  
 Query Match: 25.54% Indels: 56  
 Gaps: 7

US-08-978-217-16 (1-371) x US-09-009-913-338 (1-848)

QY 56 AlasertPrThrsSerGluArgProGlnPheTyrSerLysThrGlnValLeuGluTrpIle 75  
 DB 118 AGCCAGTGTGAGTGAATCCACCCCTGAGTGTGACCAATACAGGATGAGGATGCTG 177  
 QY 76 SerTyrGlnValGlnLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsn 95  
 DB 178 CAGCACTCTCTGGACACCAACGAGTACGCTGATCCCTTCCAGAGTTCGAC 237  
 QY 96 MetAspGlyAlaThrLeuGlnCysSerCysAlaLeuGlnLysValLeuArgLeuValPheGlyPro 115  
 DB 238 ATTACCGGAGAACACCTGTGTGACGATGATCTGACAGGATTCACAGAGGACGAGCTCA 297  
 QY 116 LeuGlyAspGlnLeuHisIleGlnLeuArgAspLeuThrSerAsn-----SerSer 132  
 DB 298 GCTGGGACAGCTCTCTGACGACCAACCTCAAGTCAATGAGACGGCCATGACAGCAGT 357  
 QY 133 AspGlnLeuSerTrpIleIleGlnLeuGlnLysAspGlyMetSerPheGlnLysSer 152  
 DB 358 GAC-----CTTTCCAGCTCCGCA 375  
 QY 153 LeuGlyAspLeuGlyProPheAspGlnLysSerProPheAlaGlnLysLeuAspAsp 172  
 DB 376 CACAAATGATTCATGTCACAGCTCAACCAACCATCTCT-----TTCATCTGAAACACA 426  
 QY 173 GlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGly 192  
 DB 427 TGGAAAGAGAAAGAACTATCTATGATCCAGCTATGTAGACAGATGATGCTGTTGAC 486  
 QY 193 SerSerAspValSerThrAlaArgThrAlaThrProGlnLysSerSerHisAlaSerAspSer 212  
 DB 487 AGTAAGACTTTCTGCGCGGCTCAGATCTCCATGACAACTCCAGTCAAC-----534  
 QY 213 GlyLysSerAspValAspLeuAspLeuThrGlnSerLysValPheProArgAspAspPhe 232  
 DB 535 -----CTTCCAGTTGCAAGTCA-----552  
 QY 233 ThrAspTyrLysLysGlyGlnProLysHisGlyLysArgLysArgGlyArgProArgLys 252  
 DB 553 CCTGATATGAAAAAG---GAGCAAGACCACT-----582  
 QY 253 LeuSerLysGluTyrTrpAspCysLeuGlnLysLysSerLysHisAlaProArgGly 272  
 DB 583 -----GTAAAGTCCACACCCMAAAAGACAAACCAAGAGGC 618  
 QY 273 ThrHisLeuTrpGlnPheIleArgAspIleLeuIleHisProGlnLeuAsnGlnLysLeu 292  
 DB 619 ACTCACTTATGGAGAGTTCCTCGAGACATCTCTTGAGCCCAAGACAAAGAACCCAGGCTG 678  
 QY 293 MetLysTrpGlnAsnArgHisGlnGlyValPheLysPheLeuArgSerGlnIleValAla 312  
 DB 679 ATCAATATGGAGAGACCGTTCGAGAGCATCTTCAGGTTCTTAAGTCATAAAGCTGTGGCT 738  
 QY 313 GlnLeuTrpGlyGlnLysLysLysSerSerAsnMetThrTyrGlnLysLeuSerArgAla 332  
 DB 739 CAGCTGTGGGGAGAAAAAGAAATAAACGTACATGACATACGAGAGAGCTCAGCGGCT 798  
 QY 333 MetArgTyrTyrTyrLysArgGlnLysLeuGlnArgValAspGlyArg 348  
 DB 799 ATGAGATATTTACTACAAACGAGAAATCTTGAAACGTGTGATGACGA 846

RESULT 12  
 US-09-009-913-8  
 ; Sequence 8, Application US/09009913  
 ; Patent No. 6087485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Axy's Pharmaceuticals, Inc.

TITLE OF INVENTION: Asthma Related Genes  
 NUMBER OF SEQUENCES: 339  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bozicevic & Reed, LLP  
 STREET: 285 Hamilton Ave, Suite 200  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,913

FILING DATE: 21-JAN-1998

CLASSIFICATION: DATA:

PRIOR APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Sherwood, Pamela J

REGISTRATION NUMBER: 36,677

REFERENCE/DOCKET NUMBER: SEQ-4P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-327-3231

TELEFAX: 650-327-3231

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 2280 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-09-009-913-8

Alignment Scores:

Pred. No.: 8,91e-37 Length: 2280

Score: 435.50 Matches: 95

Percent Similarity: 46.60% Conservative: 49

Best Local Similarity: 30.74% Mismatches: 66

Query Match: 21.94% Indels: 99

Gaps: 6

US-08-978-217-16 (1-371) x US-09-009-913-8 (1-2280)

QY 58 TrpThrsSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTrpIleSerTyr 77  
 DB 206 TGGACATCAGTCCACCCCTGAATACGTGACTAAGCCCATGTGTGGAGCTCCAGTTC 265  
 QY 78 GlnValGlnLysAsnLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAsp 97  
 DB 266 TCGTCGACACGATACAACTTGGACACCAATGACATCTCTTGCACATTCATCACTCACT 325  
 QY 98 GlyAlaTrpLysCysSerCysAlaLeuGlnLysLeuArgLeuValPheGlyProLeuGly 117  
 DB 326 GGCCTGACAGCTGTGACGATGACACAGAGAGATTCTTCGAGGACGCTGCGGCTC 385  
 QY 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGlnLeuSerTrp 137  
 DB 386 GAGTACCTGTAC-----TTC 400  
 QY 138 IleIleGlnLeuLeuGlnLysAspGlyMetSerPheGlnLysSerLeuGlyAspLeuGly 157  
 DB 401 ATCTTCAGAACATCTCCGACACCAAGGTTACTCTTT-----436  
 QY 158 ProPheAspGlnLysSerProPheAlaGlnLysLeuLeuAspAspGlyArgGlnAlaSer 177  
 DB 437 -----TTTAATGACGCTGAAGAAAGCAAG 460  
 QY 178 ProTyrTyrCysSerThrTyrGlyProGlyAlaProSerProGlySerSerAspValSer 197



Db 840 AGAAGAAAAATGACAGATATGATGATAAAAGTTGACAGAGCCCTGAGATACTAT 899  
 Qy 338 LysArgGluIleLeuGluArgValAspGlyArgLeuValIleTyrPheGlyLysAsn 357  
 Db 900 AAAACAGAAATTTTGGACCGGTTGAC---CGAAGTTAGTGTACAAATTTGGAAAAAT 956  
 Qy 358 SerSerGlyTyrPheGluGluGluVal 366  
 Db 957 GCACACGGGTGACAGAGACAGACTA 983

## RESULT 14

US-09-009-913-10  
 ; Sequence 10, Application US/09009913  
 ; Patent No. 6087485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ays Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: Asthma Related Genes  
 ; NUMBER OF SEQUENCES: 339  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Bozicevic & Reed, LLP  
 ; STREET: 285 Hamilton Ave, Suite 200  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/009,913  
 ; FILING DATE: 21-JAN-1998  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sherwood, Pamela J  
 ; REGISTRATION NUMBER: 36,677  
 ; REFERENCE/DOCKET NUMBER: SEQ-4P  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-327-3231  
 ; TELEFAX: 650-327-3231  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2498 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-09-009-913-10

## Alignment Scores:

Pred. No.: 1,03e-36 Length: 2498  
 Score: 435.50 Matches: 95  
 Percent Similarity: 46.60% Conservative: 49  
 Best Local Similarity: 30.74% Mismatches: 66  
 Query Match: 21.94% Indels: 99  
 DB: 3 Gaps: 6

US-08-978-217-16 (1-371) x US-09-009-913-10 (1-2498)

Qy 58 TrpHisSerGluArgProGlnPheTyrSerIleThrGlnValLeuGluTyrPheSerTyr 77  
 Db 423 TGGACATGATGCCACCCCTGAATGACTAAGCCCATGTGTGGAGTGGCTCCAGTTTC 482  
 Qy 78 GlnValGluIleLeuGluArgValAspGlyArgLeuValIleTyrPheGlyLysAsn 97  
 Db 483 TGCTGGACACGATGACAGTGGACCAATGATGCTCTTCTGCAACTTCAACATCAGT 542

Qy 98 GlyAlaThrIleLeuCysSerCysAlaLeuGluIleLeuArgLeuValIlePheGlyProLeuGly 117  
 Db 543 GGCTTGACAGCTGTGCACCATGACACAGAGAGTTCCTCGAGGACGCTGCTCGGCG 602  
 Qy 118 AspGlnLeuHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerTyr 137  
 Db 603 GAGTACTCTGAC-----TTC 617  
 Qy 138 IleIleGlnLeuLeuGluLysAspGlyMetSerPheGlnGlnSerLeuGlyAspLeuGly 157  
 Db 618 ATCTCCAGACATCCGACACAGAGTTACTCTTT----- 653  
 Qy 158 ProPheAspGlnGlySerProPheAlaGlnIleLeuLeuAspAspGlyArgGlnAlaSer 177  
 Db 654 -----TTTAATGACCGCTGAAGAACAG 677  
 Qy 178 ProTyrTyrCysSerThrTyrGlyProGlyValAlaProSerProGlySerSerAspValSer 197  
 Db 678 -----GCCACATCAAGACTGCTGATTTCCAC 707  
 Qy 198 ThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGlySerAspVal 217  
 Db 708 TGCTTGAACACAGTGGCATCAAAAGTCAA----- 737  
 Qy 218 AspLeuAspLeuThrGlnSerIleValPheProArgAspAspPheThrAspTyrIleLys 237  
 Db 737 ----- 737  
 Qy 238 GlyGluProLysHisGlyLysArgLysArgGlyValArgProArgLysLeuSerLysGluTyr 257  
 Db 737 ----- 737  
 Qy 258 TrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGlu 277  
 Db 738 ---GACTGT-----CACAGTCATAGTAGAACAGCCCTCAAGTTCATCTATGGAA 788  
 Qy 278 PheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysTrpGluAsn 297  
 Db 789 TTTGACGAGACCTGCTTCTATCTCTGAAAGAAACCTGTGCATCTCGAATGGAAAGAT 848  
 Qy 298 ArgHisGluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTyrGln 317  
 Db 849 AGGAAACAGGAATTTTTCGGGTGTTAAATCGAAGCCCTCGCAACATGTGGGACAA 908  
 Qy 318 LysLysLysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMetArgTyrTyr 337  
 Db 909 AGAAGAAAAATGACAGATGACGTATGAAAAGTTGACAGAGCCCTGAGATACTAT 968  
 Qy 338 LysArgGluIleLeuGluArgValAspGlyArgLeuValIleTyrPheGlyLysAsn 357  
 Db 969 AAAACAGGAATTTTGGACCGGTTGAC---CGAAGTTAGTGTACAAATTTGAAAAAAT 1025  
 Qy 358 SerSerGlyTyrPheGluGluGluVal 366  
 Db 1026 GCACACGGGTGACAGAGACAGACTA 1052

## RESULT 15

US-08-368-281-1  
 ; Sequence 1, Application US/08368281  
 ; Patent No. 5721113  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Libermann, Towia A  
 ; APPLICANT: Oetgen, Joerg P  
 ; APPLICANT: Kunsch, Charles A  
 ; TITLE OF INVENTION: NERF Genes  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road  
 ; CITY: King of Prussia  
 ; STATE: Pennsylvania  
 ; COUNTRY: USA  
 ; ZIP: 19406

```

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MC-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,281
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2975 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

```

